



1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/686,346B

DATE: 04/08/2004
 TIME: 16:10:19

Input Set : D:\Utsd1276.app
 Output Set: N:\CRF4\04082004\I686346B.raw

PG. 6

3 <110> APPLICANT: COBB, MELANIE
 4 HUTCHISON, MICHELE
 5 ZHU, CHEN
 6 BERMAN, KEVIN
 8 <120> TITLE OF INVENTION: TAO PROTEIN KINASE POLYPEPTIDES AND METHODS OF USE
 9 THEREFOR
 11 <130> FILE REFERENCE: UTSD:1276USC1
 13 <140> CURRENT APPLICATION NUMBER: 09/686,346B
 14 <141> CURRENT FILING DATE: 2000-10-10
 16 <150> PRIOR APPLICATION NUMBER: 09/060,410
 17 <151> PRIOR FILING DATE: 1998-04-14
 19 <160> NUMBER OF SEQ ID NOS: 28
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 3312
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Rattus norvegicus
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (121)..(3123)
 32 <400> SEQUENCE: 1
 33 tctgcagttat tatttatgca tttatgccag tgtggcttca ttcatacaga 60
 35 tgaaccaago tttgggatag cagtataaaa tttagaatcag acagctgact gctcagcagg 120
 37 atg cca tca act aac aga gca ggc agt cta aag gac cct gaa atc gca 168
 38 Met Pro Ser Thr Asn Arg Ala Gly Ser Leu Lys Asp Pro Glu Ile Ala
 39 1 5 10 15
 41 gag ctc ttc ttc aaa gaa gat ccg gaa aaa ctc ttc aca gat ctc aga 216
 42 Glu Leu Phe Phe Lys Glu Asp Pro Glu Lys Leu Phe Thr Asp Leu Arg
 43 20 25 30
 45 gaa atc ggc cat ggg agc ttt gga gca gtt tat ttt gca cga gat gtg 264
 46 Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Arg Asp Val
 47 35 40 45
 49 cgt act aat gaa gtg gtg gcc atc aag aaa atg tct tat agt gga aag 312
 50 Arg Thr Asn Glu Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys
 51 50 55 60
 53 cag tct act gag aaa tgg cag gat att att aag gaa gtc aag ttt cta 360
 54 Gln Ser Thr Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Lys Phe Leu
 55 65 70 75 80
 57 caa aga ata aaa cat ccc aac agt ata gaa tac aaa ggc tgc tat tta 408
 58 Gln Arg Ile Lys His Pro Asn Ser Ile Glu Tyr Lys Gly Cys Tyr Leu
 59 85 90 95
 61 cgt gaa cac aca gca tgg ctt gta atg gaa tat tgt tta gga tct gct 456
 62 Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala

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63	100	105	110	
65	tcg gat tta cta gaa gtt cat aaa aag cca tta caa gaa gtg gaa ata			504
66	Ser Asp Leu Leu Glu Val His Lys Lys Pro Leu Gln Glu Val Glu Ile			
67	115	120	125	
69	gca gca att aca cat ggt gct ctc cag gga tta gct tat tta cat tct			552
70	Ala Ala Ile Thr His Gly Ala Leu Gln Gly Leu Ala Tyr Leu His Ser			
71	130	135	140	
73	cat acc atg atc cat aga gat atc aaa gca gga aat atc ctt ctg aca			600
74	His Thr Met Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Thr			
75	145	150	155	160
77	gaa cca ggc caa gtg aaa ctt gct gac ttt gga tct gct tcc atg gcc			648
78	Glu Pro Gly Gln Val Lys Leu Ala Asp Phe Gly Ser Ala Ser Met Ala			
79	165	170	175	
81	tcc cct gcc aat tct ttt gtg gga aca cca tat tgg atg gcc cca gaa			696
82	Ser Pro Ala Asn Ser Phe Val Gly Thr Pro Tyr Trp Met Ala Pro Glu			
83	180	185	190	
85	gta att tta gcc atg gat gaa gga caa tat gat ggc aaa gtt gat gta			744
86	Val Ile Leu Ala Met Asp Glu Gly Gln Tyr Asp Gly Lys Val Asp Val			
87	195	200	205	
89	tgg tct ctt gga ata aca tgt att gaa tta gcc gag agg aag cct cct			792
90	Trp Ser Leu Gly Ile Thr Cys Ile Glu Leu Ala Glu Arg Lys Pro Pro			
91	210	215	220	
93	tta ttt aat atg aat gca atg agt gcc tta tat cac ata gcc caa aat			840
94	Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile Ala Gln Asn			
95	225	230	235	240
97	gaa tcc cct aca cta cag tct aat gaa tgg tct gat tat ttt cga aac			888
98	Glu Ser Pro Thr Leu Gln Ser Asn Glu Trp Ser Asp Tyr Phe Arg Asn			
99	245	250	255	
101	ttt gta gat tct tgc ctc cag aaa atc cct caa gat cgc cct aca tca			936
102	Phe Val Asp Ser Cys Leu Gln Lys Ile Pro Gln Asp Arg Pro Thr Ser			
103	260	265	270	
105	gag gaa ctt tta aag cac atg ttt gtt ctt cga gag cgc cct gaa aca			984
106	Glu Glu Leu Leu Lys His Met Phe Val Leu Arg Glu Arg Pro Glu Thr			
107	275	280	285	
109	gtg tta ata gat ctt att caa agg aca aag gat gca gta aga gag ctg			1032
110	Val Leu Ile Asp Leu Ile Gln Arg Thr Lys Asp Ala Val Arg Glu Leu			
111	290	295	300	
113	gac aat cta caa tat cga aag atg aag aaa ctc ctt ttc cag gag gca			1080
114	Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Leu Leu Phe Gln Glu Ala			
115	305	310	315	320
117	cat aat gga cca gca gta gaa gca cag gaa gaa gag gag gag caa gat			1128
118	His Asn Gly Pro Ala Val Glu Ala Gln Glu Glu Glu Glu Gln Asp			
119	325	330	335	
121	cat ggt ggt ggc cgg aca gga aca gta aat agt gtt gga agc aat cag			1176
122	His Gly Gly Arg Thr Gly Thr Val Asn Ser Val Gly Ser Asn Gln			
123	340	345	350	
125	tct atc ccc agt atg tct atc agt gcc agt agc caa agc agc agt gtt			1224
126	Ser Ile Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser Ser Ser Val			
127	355	360	365	

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129 aat agt ctt cca gat gca tcg gat gac aag agt gag cta gac atg atg	1272
130 Asn Ser Leu Pro Asp Ala Ser Asp Asp Lys Ser Glu Leu Asp Met Met	
131 370 375 380	
133 gag gga gac cat aca gtg atg tct aac agt tct gtc atc cac tta aaa	1320
134 Glu Gly Asp His Thr Val Met Ser Asn Ser Ser Val Ile His Leu Lys	
135 385 390 395 400	
137 cct gag gag gaa aat tac caa gaa gaa gga gat cct aga aca aga gca	1368
138 Pro Glu Glu Glu Asn Tyr Gln Glu Gly Asp Pro Arg Thr Arg Ala	
139 405 410 415	
141 tca gct cca cag tct cca ctt gtg tct cgt cac aaa tca cat tat	1416
142 Ser Ala Pro Gln Ser Pro Pro Gln Val Ser Arg His Lys Ser His Tyr	
143 420 425 430	
145 cgt aat aga gaa cac ttt gca act ata cga aca gca tca ctg gtt aca	1464
146 Arg Asn Arg Glu His Phe Ala Thr Ile Arg Thr Ala Ser Leu Val Thr	
147 435 440 445	
149 aga cag atg caa gaa cat gag cag gac tct gaa ctt aga gaa cag atg	1512
150 Arg Gln Met Gln Glu His Gln Asp Ser Glu Leu Arg Glu Gln Met	
151 450 455 460	
153 tct ggt tat aag cgg atg agg cga cag cat cag aag cag ctg atg act	1560
154 Ser Gly Tyr Lys Arg Met Arg Arg Gln His Gln Lys Gln Leu Met Thr	
155 465 470 475 480	
157 ctg gaa aat aaa ctg aag gca gaa atg gac gaa cat cgg ctc aga tta	1608
158 Leu Glu Asn Lys Leu Lys Ala Glu Met Asp Glu His Arg Leu Arg Leu	
159 485 490 495	
161 gac aaa gat ctt gaa act cag cgc aac aat ttc gct gca gaa atg gag	1656
162 Asp Lys Asp Leu Glu Thr Gln Arg Asn Asn Phe Ala Ala Glu Met Glu	
163 500 505 510	
165 aaa ctt att aag aaa cac caa gct tct atg gaa aaa gag gct aaa gtg	1704
166 Lys Leu Ile Lys Lys His Gln Ala Ser Met Glu Lys Glu Ala Lys Val	
167 515 520 525	
169 atg gcc aac gag gag aaa aaa ttc caa caa cac att cag gct caa cag	1752
170 Met Ala Asn Glu Glu Lys Lys Phe Gln Gln His Ile Gln Ala Gln Gln	
171 530 535 540	
173 aag aaa gaa ctg aat agc ttt ttg gag tct caa aaa aga gaa tat aaa	1800
174 Lys Lys Glu Leu Asn Ser Phe Leu Glu Ser Gln Lys Arg Glu Tyr Lys	
175 545 550 555 560	
177 ctt cga aaa gag cag ctt aag gag gag ctg aat gaa aac cag agc aca	1848
178 Leu Arg Lys Glu Gln Leu Lys Glu Glu Leu Asn Glu Asn Gln Ser Thr	
179 565 570 575	
181 cct aaa aaa gaa aag cag gaa tgg ctt tca aag cag aag gag aat att	1896
182 Pro Lys Lys Glu Lys Gln Glu Trp Leu Ser Lys Gln Lys Glu Asn Ile	
183 580 585 590	
185 caa cat ttt cag gca gaa gaa gaa gct aat ctt ctt cga cgt caa agg	1944
186 Gln His Phe Gln Ala Glu Glu Ala Asn Leu Leu Arg Arg Gln Arg	
187 595 600 605	
189 cag tat cta gag cta gaa tgt cgt cgc ttc aaa aga aga atg tta ctt	1992
190 Gln Tyr Leu Glu Leu Glu Cys Arg Arg Phe Lys Arg Arg Met Leu Leu	
191 610 615 620	
193 ggt cgg cat aac ttg gaa cag gac ctt gtc agg gag gag tta aac aaa	2040

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194	Gly Arg His Asn Leu Glu Gln Asp Leu Val Arg Glu Glu Leu Asn Lys				
195	625	630	635	640	
197	agg cag act cag aag gac tta gaa cat gca atg tta ctg cga cag cat	2088			
198	Arg Gln Thr Gln Lys Asp Leu Glu His Ala Met Leu Leu Arg Gln His				
199	645	650	655		
201	gaa tcc atg caa gaa ctg gag ttt cgc cac ctc aac act att cag aag	2136			
202	Glu Ser Met Gln Glu Leu Glu Phe Arg His Leu Asn Thr Ile Gln Lys				
203	660	665	670		
205	atg cgc tgt gag ttg atc aga ctg caa cat caa act gag ctt act aac	2184			
206	Met Arg Cys Glu Leu Ile Arg Leu Gln His Gln Thr Glu Leu Thr Asn				
207	675	680	685		
209	cag ctg gaa tac aat aag aga agg gaa cgg gaa cta aga cgg aaa cat	2232			
210	Gln Leu Glu Tyr Asn Lys Arg Arg Glu Arg Glu Leu Arg Arg Lys His				
211	690	695	700		
213	gtc atg gaa gtt cga cag cag cct aag agt ttg aag tct aaa gaa ctc	2280			
214	Val Met Glu Val Arg Gln Gln Pro Lys Ser Leu Lys Ser Lys Glu Leu				
215	705	710	715	720	
217	caa ata aaa aag cag ttt cag gat acc tgc aaa att caa acc aga cag	2328			
218	Gln Ile Lys Lys Gln Phe Gln Asp Thr Cys Lys Ile Gln Thr Arg Gln				
219	725	730	735		
221	tac aaa gca tta agg aat cac cta ctg gag act aca cca aag agt gag	2376			
222	Tyr Lys Ala Leu Arg Asn His Leu Leu Glu Thr Thr Pro Lys Ser Glu				
223	740	745	750		
225	cac aaa gct gtt ctg aaa aga ctc aag gag gaa cag act cgg aag tta	2424			
226	His Lys Ala Val Leu Lys Arg Leu Lys Glu Glu Gln Thr Arg Lys Leu				
227	755	760	765		
229	gcc atc ttg gct gag cag tat gat cat agc att aat gaa atg ctc tcc	2472			
230	Ala Ile Leu Ala Glu Gln Tyr Asp His Ser Ile Asn Glu Met Leu Ser				
231	770	775	780		
233	aca caa gct ctg cgt ttg gat gaa gca cag gaa gca gaa tgc cag gtt	2520			
234	Thr Gln Ala Leu Arg Leu Asp Glu Ala Gln Glu Ala Glu Cys Gln Val				
235	785	790	795	800	
237	ttg aag atg cag cta cag cag gaa ctg gag ctg ttg aat gca tat cag	2568			
238	Leu Lys Met Gln Leu Gln Glu Leu Glu Leu Leu Asn Ala Tyr Gln				
239	805	810	815		
241	agc aaa atc aag atg cag gct gag gcc caa cat gat cga gag ctt cga	2616			
242	Ser Lys Ile Lys Met Gln Ala Glu Ala Gln His Asp Arg Glu Leu Arg				
243	820	825	830		
245	gag ctg gaa caa agg gtc tcc ctt cgg aga gca ctc tta gaa cag aag	2664			
246	Glu Leu Glu Gln Arg Val Ser Leu Arg Arg Ala Leu Leu Glu Gln Lys				
247	835	840	845		
249	att gaa gaa gag atg ttg gct ttg cag aat gaa cgc aca gaa cga ata	2712			
250	Ile Glu Glu Glu Met Leu Ala Leu Gln Asn Glu Arg Thr Glu Arg Ile				
251	850	855	860		
253	cgt agc ctg ctc gag cgc cag gcc aga gaa att gaa gct ttt gac tct	2760			
254	Arg Ser Leu Leu Glu Arg Gln Ala Arg Glu Ile Glu Ala Phe Asp Ser				
255	865	870	875	880	
257	gaa agc atg aga tta ggt ttt agt aac atg gtc ctt tct aat ctc tcc	2808			
258	Glu Ser Met Arg Leu Gly Phe Ser Asn Met Val Leu Ser Asn Leu Ser				

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259	885	890	895	
261	cct gag gca ttc agc cac agc tac cca gga gct tct agc tgg tct cac			2856
262	Pro Glu Ala Phe Ser His Ser Tyr Pro Gly Ala Ser Ser Trp Ser His			
263	900	905	910	
265	aat cct act ggg ggt tca gga cct cac tgg ggt cat ccc atg ggt ggc			2904
266	Asn Pro Thr Gly Gly Ser Gly Pro His Trp Gly His Pro Met Gly Gly			
267	915	920	925	
269	aca cca caa gct tgg ggt cat ccg atg caa ggc gga ccc caa cca tgg			2952
270	Thr Pro Gln Ala Trp Gly His Pro Met Gln Gly Gly Pro Gln Pro Trp			
271	930	935	940	
273	ggt cac ccc tca ggg cca atg caa ggg gta cct cga ggt agc agt ata			3000
274	Gly His Pro Ser Gly Pro Met Gln Gly Val Pro Arg Gly Ser Ser Ile			
275	945	950	955	960
277	gga gtc cgc aat agc ccc cag gct ctg agg cgg aca gct tct ggg gga			3048
278	Gly Val Arg Asn Ser Pro Gln Ala Leu Arg Arg Thr Ala Ser Gly Gly			
279	965	970	975	
281	cgg acg gaa cag ggc atg agc aga agc acg agt gtc act tca caa ata			3096
282	Arg Thr Glu Gln Gly Met Ser Arg Ser Thr Ser Val Thr Ser Gln Ile			
283	980	985	990	
285	tcc aat ggg tca cac atg tct tac aca taataattga aagtggcaat			3143
286	Ser Asn Gly Ser His Met Ser Tyr Thr			
287	995	1000		
289	tccgctggag ctgtctgcca aaagaaaactg cctacagaca tcagcacagc agcctcctca			3203
291	cttgggtact accgggtgga agctgtgcat atggatatatt ttattcgctt ttgtaaagcg			3263
293	ttatgtttt tgtttactaa ttgggatgtc atagtatgg gctgccggg			3312
296	<210> SEQ ID NO: 2			
297	<211> LENGTH: 1001			
298	<212> TYPE: PRT			
299	<213> ORGANISM: Rattus norvegicus			
301	<400> SEQUENCE: 2			
302	Met Pro Ser Thr Asn Arg Ala Gly Ser Leu Lys Asp Pro Glu Ile Ala			
303	1	5	10	15
305	Glu Leu Phe Phe Lys Glu Asp Pro Glu Lys Leu Phe Thr Asp Leu Arg			
306	20	25	30	
308	Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Arg Asp Val			
309	35	40	45	
311	Arg Thr Asn Glu Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys			
312	50	55	60	
314	Gln Ser Thr Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Lys Phe Leu			
315	65	70	75	80
317	Gln Arg Ile Lys His Pro Asn Ser Ile Glu Tyr Lys Gly Cys Tyr Leu			
318	85	90	95	
320	Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala			
321	100	105	110	
323	Ser Asp Leu Leu Glu Val His Lys Lys Pro Leu Gln Glu Val Glu Ile			
324	115	120	125	
326	Ala Ala Ile Thr His Gly Ala Leu Gln Gly Leu Ala Tyr Leu His Ser			
327	130	135	140	
329	His Thr Met Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Thr			

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/08/2004
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 5,92,138
Seq#:7; N Pos. 208,210,223
Seq#:10; N Pos. 192
Seq#:11; N Pos. 18
Seq#:19; N Pos. 24,31
Seq#:20; N Pos. 3,6,13,16,19
Seq#:21; N Pos. 11,14,18
Seq#:22; N Pos. 19,22

VERIFICATION SUMMARY
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L:1012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
M:341 Repeated in SeqNo=5
L:1049 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:180
L:1091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:180
L:1105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:1296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:1314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:1332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:1350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0